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海洋巨大ウイルス宿主同定に関する研究
Study on the host identification of giant viruses

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研究成果概要

Megaviridae, also termed as the Giant virus, is a family of viruses proposed to infect mainly protists. Large genomes (280kb-1.51Mb) and particles (140nm-1μm) make them unique in nature. The evolutional origin and the ecological function of Megaviridae are attractive but mysterious. With the development of sequencing and omics, it has been demonstrated Megaviridae is abundant and diverse in the oceans, the diversity of which is three orders magnitude greater than the number of their hosts to date. “What do they infect?” is a challenge faced with us.

In regard to hosts identification of giant viruses, I make use of the SuperComputer System of Institute for Chemical Research, Kyoto University. Mainly, I focus on the Megaviridae, as well as other NCLDVs and their eukaryotic host candidates from TARA oceans data *in silico*. In this project, I need to use various software and packages to do deal with short reads sequences, to alignment the different sequences and reconstruct phylogenetic trees, and to conduct the co-occurrence analyses.

発表論文（謝辞あり）

発表論文（謝辞なし）